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Permanent draft genome of ´*Rhodopirellula islandica*´ strain K833

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Abstract

The ´*Rhodopirellula islandica*´ strain K833 has a lower temperature range for growth than other

genome-sequenced *Rhodopirellula baltica* and *´Rhodopirellula europaea´* strains. The draft genome of K833 was obtained as part of a larger study on the biogeography of *Rhodopirellula* species in European marine waters. The genome consists of 70 contigs with a genome size of 7439654 bp. With an average nucleotide identity of XXX % to related genomes of *Rhodopirellula baltica* and *´Rhodopirellula europaea´*, it will be a valuable source for the study of temperature adaptation of planctomycetes.

Introduction

Rhodopirellula is a genus of marine *Planctomycetes* which are unusual bacteria lacking a peptidoglycan membrane. *Planctomycetes* live frequently attached to surfaces, they are abundant in the particulate fractions of marine ecosystems and considered as important participants in the global carbon and nitrogen cycles. *Rhodopirellula baltica* SH1(T) was the source for the first planctomycete genome (Glöckner et al. 2003). A collection of 70 *Rhodopirellula* strains obtained from different European seas (Winkelmann and Harder, 2009) revealed 13 distinct operational taxonomic units (OTUs). (Winkelmann et al., 2010). Eight strains were sequenced and covered sample sites from the Baltic Sea to the Mediterranean Sea (Klindworth et al., 2014, Richter et al., 2014a,b, Richter-Heitmann et al., 2014, Wegner et al., 2014). *´Rhodopirellula islandica´* strain K833 (= JCM 17612 = DSM 24040) was isolated from a water sample on the coast of Sandgerdi, Island (64.0356 N 22.6986 W) (Winkelmann and Harder, 2009). In a comparative growth study with cells grown on M13a plates in 250ml flasks that contained 50 ml of M13 medium in artificial seawater at ~ 35 per mille salinity and were shaken at 50 rpm in the dark at 7, 14, 21, 28 or 35 °C, K833 grew in contrast to the other strains not at 35 °C, whereas *Rhodopirellula baltica* SH1(T) grew and *´Rhodopirellula europaea´* 6C had the highest growth rate at 35 °C. At 14 °C, 6C had a long lag phase before growth started and K833 had of the three strains the fastest growth rate. Thus, the strains are a valuable source for the investigation of temperature adaptation of microorganisms. The average nucleotide identity between these strains is XXXX, indicating a very close relationship between the three species.

Data description

Genomic DNA of K833 was sequenced by the Illumina MiSeq technology at the Max Planck-Genome-centre Cologne. 5494521 paired-end reads of 250 bp were dynamically trimmed with SolexaQA v.2.2. (Cox et al. 2010) and normalized with khmer 1.0 (Crusoe et al. 2014). 1462500 high-quality reads were assembled with Spades 3.1.0linux (Bankevich 2012). Contigs were *de-novo* assembled in Geneious R8 (Biomatters, Auckland, New Zealand) to remove duplications and reads were mapped with BBtools to identify possible contig elongations. The mapping reads were reassembled using the first assembly as trusted assembly in Spades. After six rounds, the assembly was stable and CheckM 0.9 indicated a completeness of 99.93% with a contamination value of 0.0 % (Parks et al. 2014). The genome was annotated in RAST (Aziz et al. 2008).

Michael – ergänzungen - literatur

The genome encodes XXXX proteins, xxx tRNAs and xxx rRNAs. These values are in the range of previously reported *Rhodopirellula* strains, with over 7 Mb and 6000 predicted open reading frames each, and reflects the complex lifestyle of the planctomycetes. Pairwise analysis by reciprocal best match BLAST revealed 4241 shared genes between the strain and *R. baltica* SH1^{T}. This high number reflects the close relation between the two species as predicted by 16S rDNA and ANI analysis. The sessile lifestyle of planctomycetes comprises life in oxygen-limited biofilms. The K833 genome codes for the synthesis of menaquinon, the typical quinon of microaerophiles, and a menaquinon (vitamin K)-dependent gamma-carboxylase that is not present in *R. baltica* SH1^{T}. The genome of K833 codes not only for cbb_3-type cytochrome c and cytochrome d oxidases – well known for their high affinity to molecular oxygen -, but also for a periplasmatic nitrate reduction pathway as alternative electron acceptor which is lacking in *R. baltica* SH1^{T}. Thus, the bacterium is well adapted to microoxic-anoxic transistion zones. A feature of these transition zones is fermentation yielding an acidification. In contrast to the *R. baltica* SH1^{T}, the K833 genome contains a glutamate decarboxylase (EC 4.1.1.15) conferring acid-resistance. It has also some unique sulfatases and glycosyl hydrolases. Unusual is the presence of *traG* and *traI* genes within a region of hypothetical proteins, indicating a

potential for genetic transfer.

Nucleotide sequence accession number. The Whole Genome Shotgun projects was deposited in INSDC (DDBJ/EBI-ENA/GenBank) under the accession number XXXXXXX.

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